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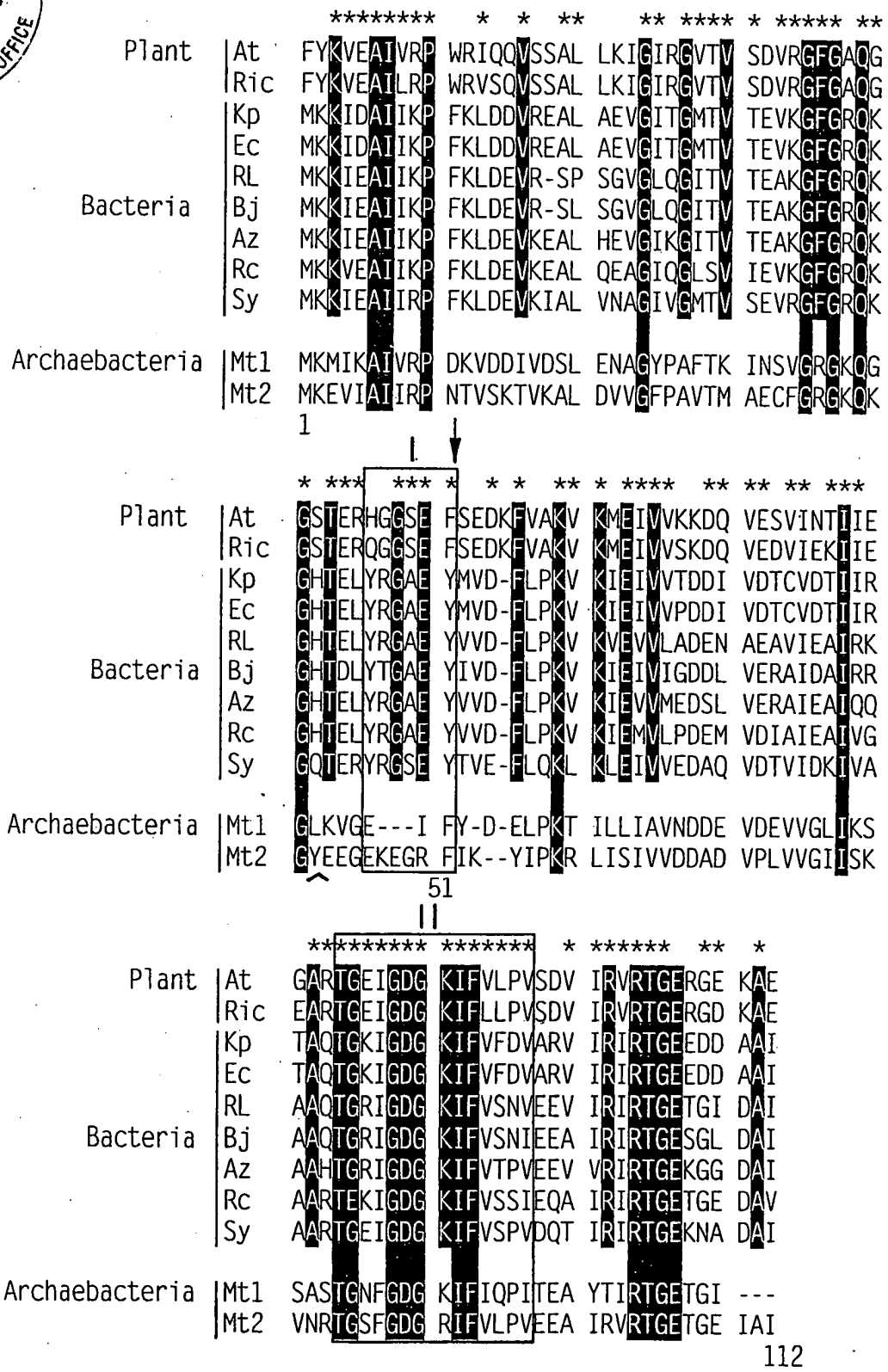

FIG. 1A

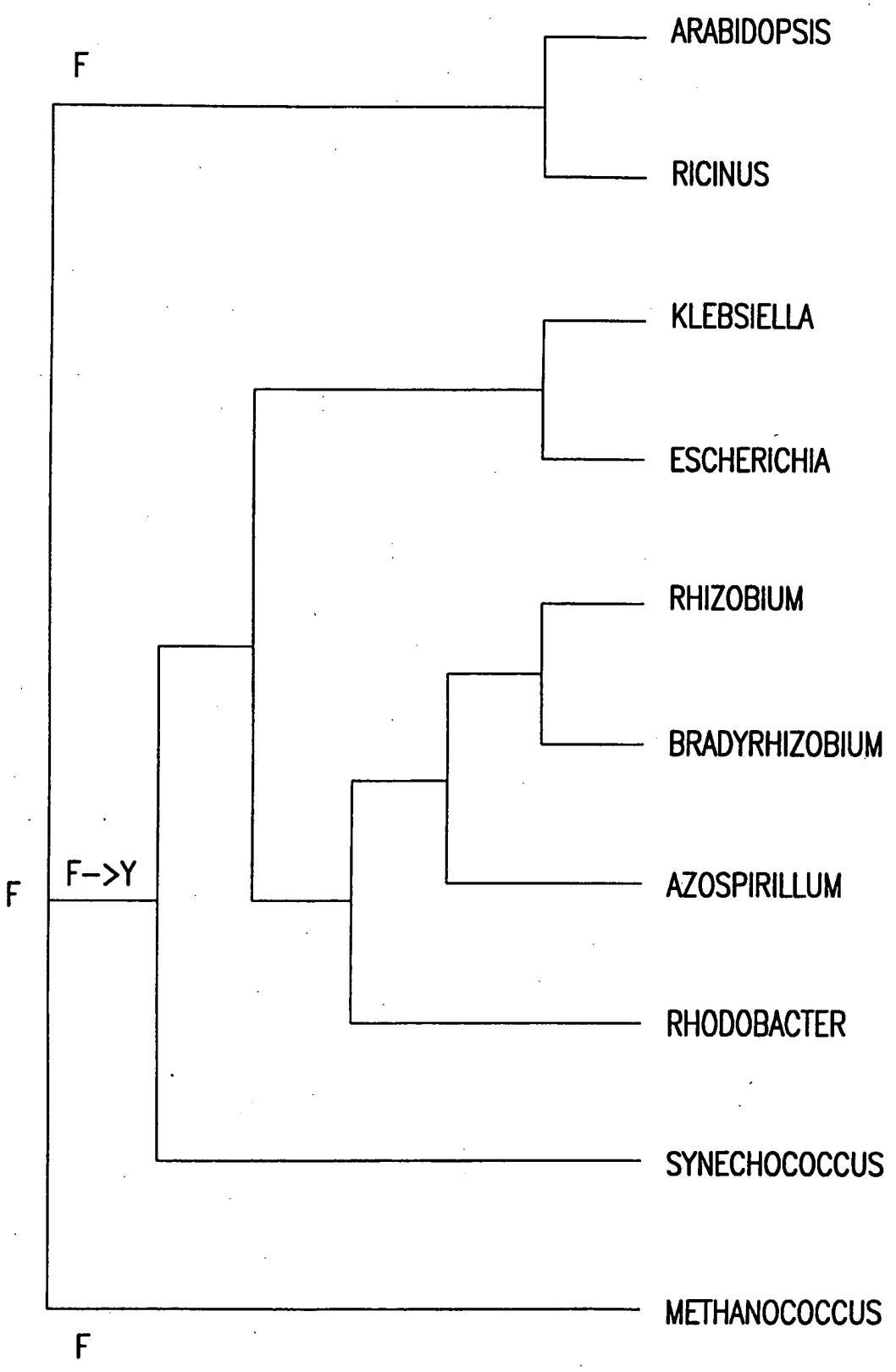

FIG. 1B

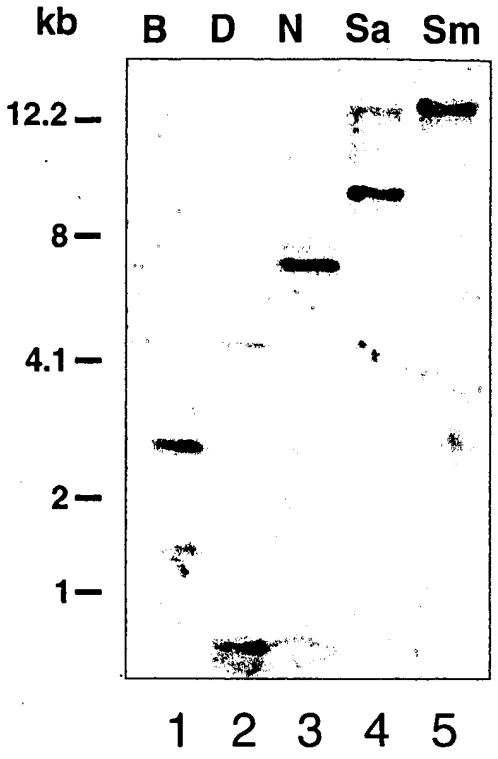

FIG.2

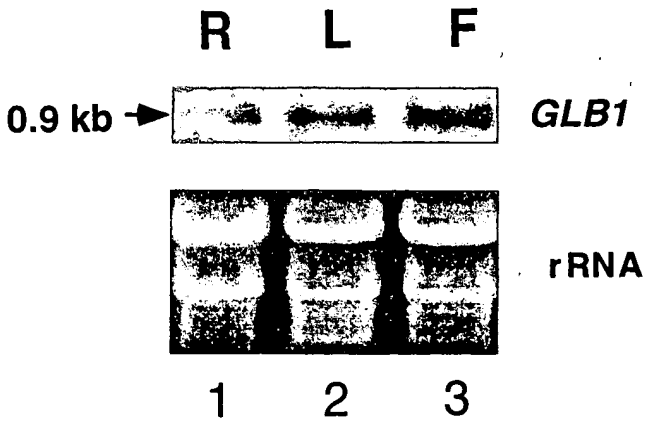

FIG.3

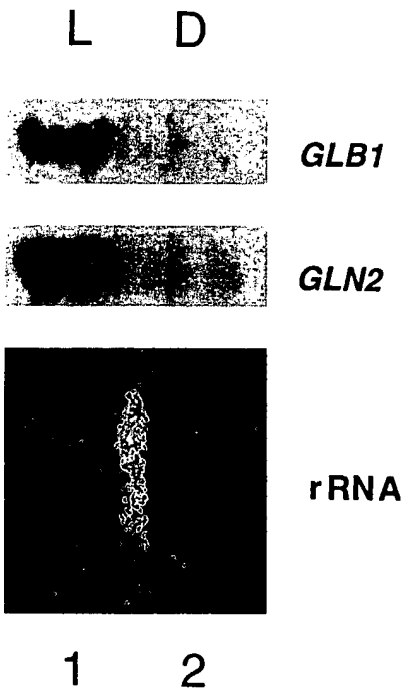

FIG.4A

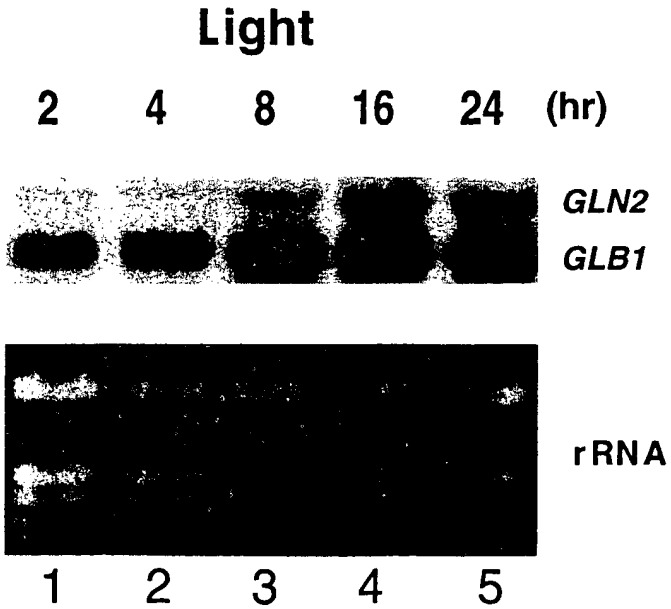

FIG.4B

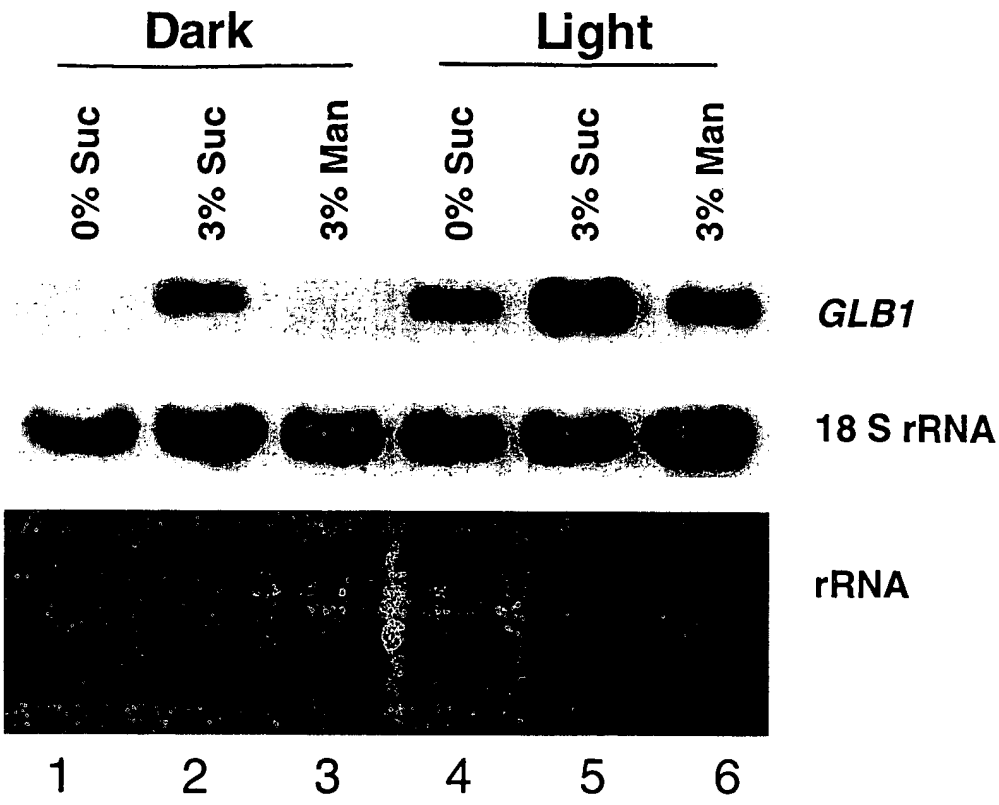

FIG.5

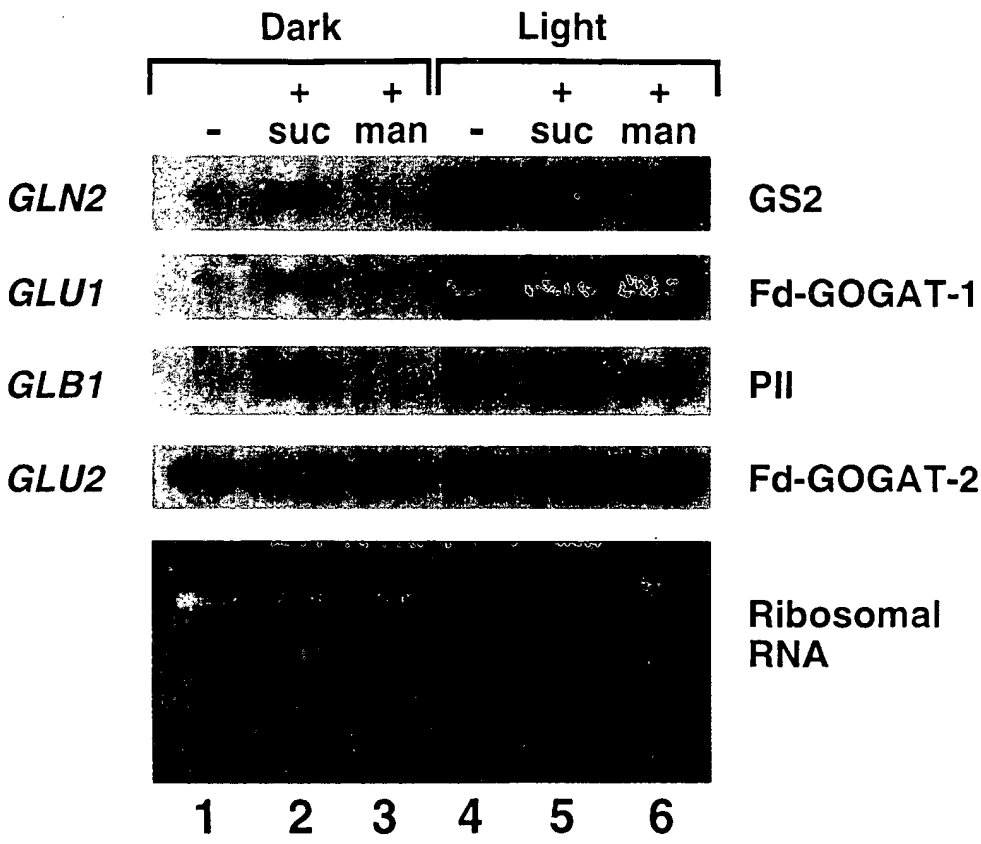

FIG.6

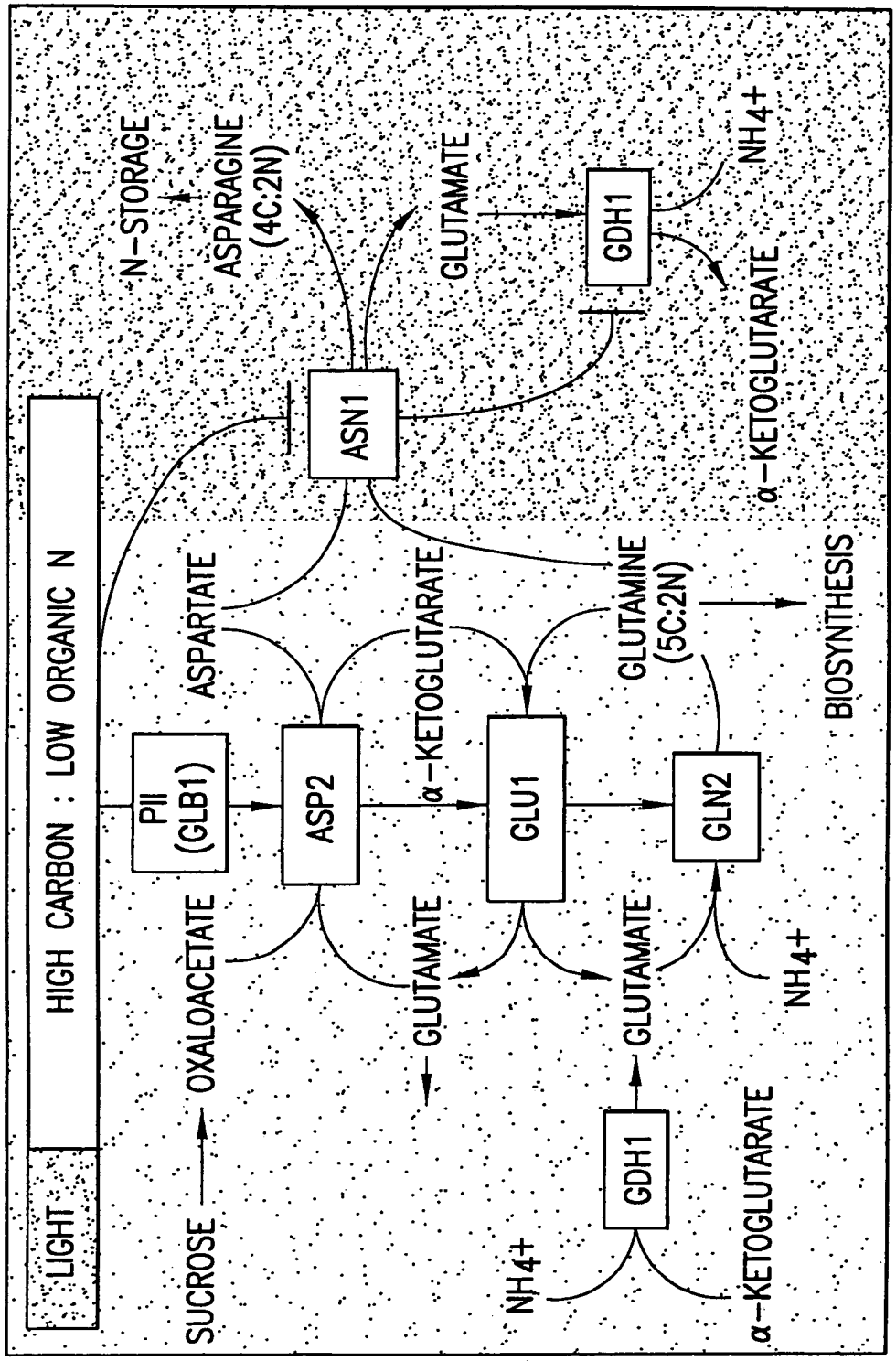

FIG. 7

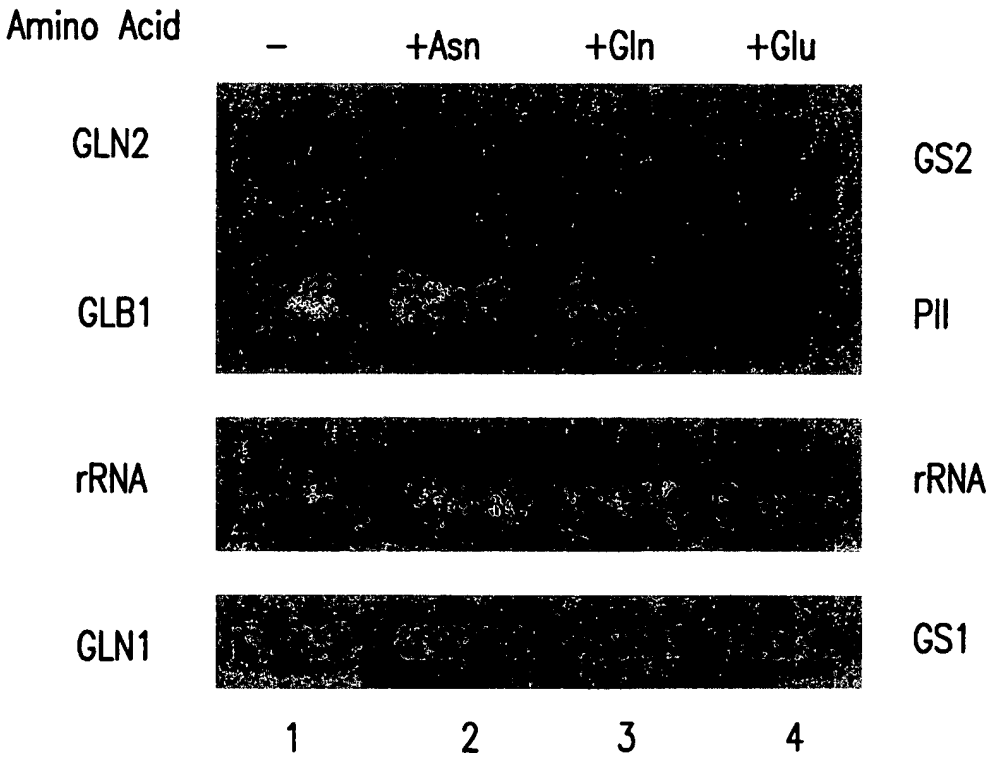

FIG.8

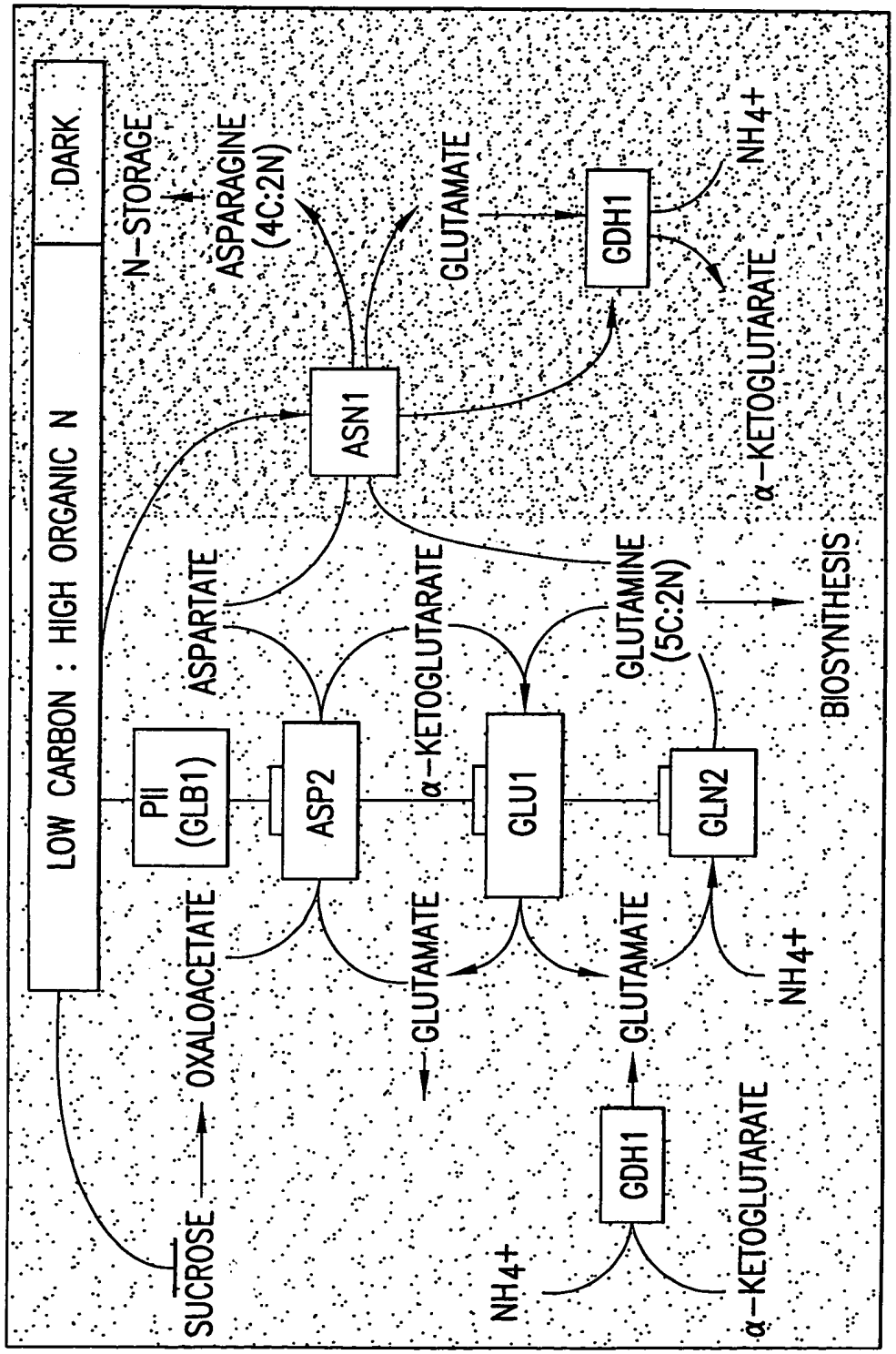

FIG.9

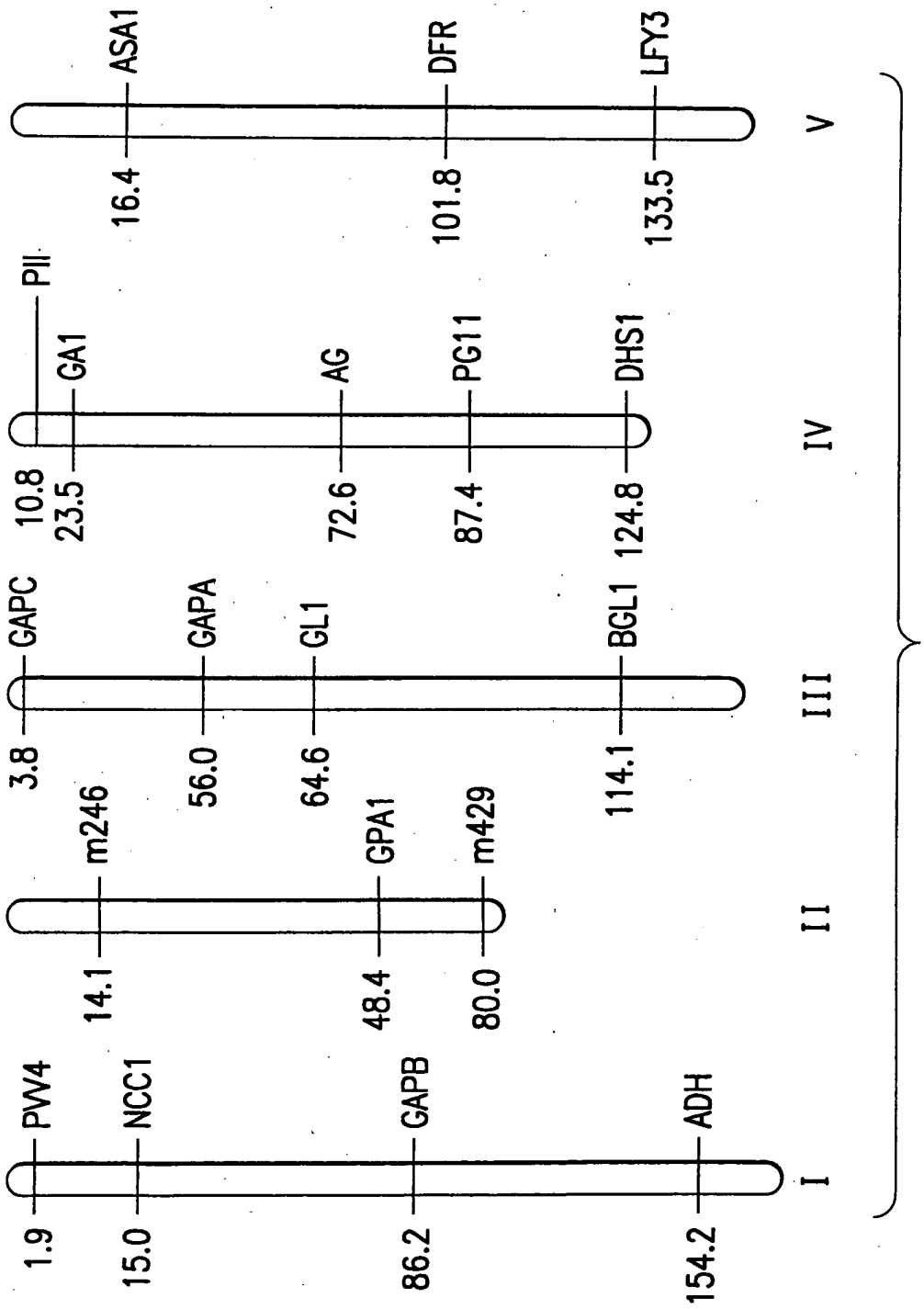

FIG.10

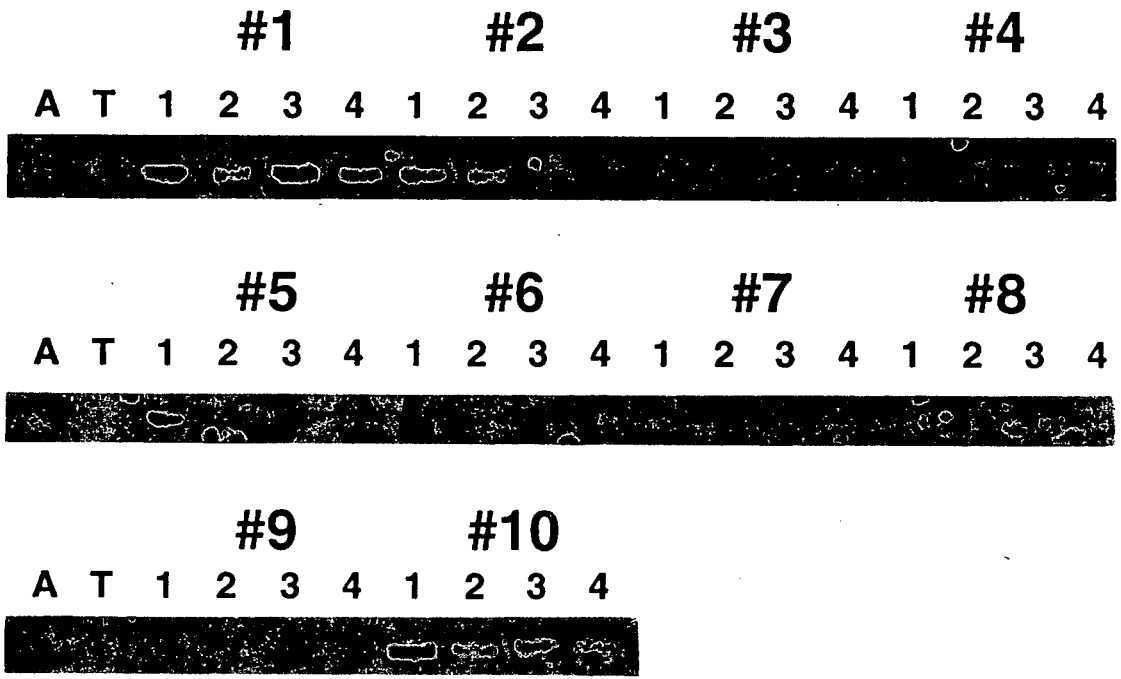

FIG.11

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 101  tgctttctct gattgcattt cgatttgttc tggattcaga cattcccgac
 151  catcttgcct cgatttggtc acaaagtcac cgagtaataa cagtcgtgtt
 201  ttacctgtcg ttagtgccca aatatcttct gattatattc cagactcgaa
 251  attttacaag gtggaagcaa ttgtcagacc atggagaatc cagcaagttt
 301  catcggcttt actgaaaatc gggattcgag gtgttactgt ttctgatgtg
 351  agagggtttg gtgcacaagg aggttctacc gagagacacg gtggctctga
 401  gttctcggaa gacaaatttg ttgctaaagt taagatggaa atcgttgtta
 451  agaaagacca agtggaatct gtaatcaaca caataattga aggagcaagg
 501  acaggagaga ttggtgatgg caagattttt gttttgcctg tgtcagatgt
 551  cataagagtt aggacaggtg agcgtgggga gaaagcagag aagatgactg
 601  gtgatatgct ttcaccgtct taggaacaaa cagagctcaa gaatggtttt
 651  ttttttttc atttcggtct ctagattctg cgaataataa tgaatggagt
 701  ctgtgtttgg tttcatgttg aatcgatcaa gatgtgtttt taactgtaca
 751  tgaattatgc agaaacatct gtcctggttc tcagacatcg aaactctgtt
 801  cctaataaaa aaaaaaa
```

FIG.12

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   1  GCGGTGTCGG CCGCTCTAGA ACTAGTGGAT CCCCCGGGCT GCAGGAATTC
  51  GGCACGAGGC TACTGCGAAA CTGGGCTTGC TCACTCCTCT TCATTCTAAT
 101  AACATCAAGA AAGAATTCCC TGTTTTTGAT TTCAGTTTGT TTTGTCCAGA
 151  GCTTAGACAT TCTCGGTTTT CTCACTTTAA CACCGCGGTC AAGCGCGTAA
 201  GATATGCCCC CGTCGTTCCT GTGATTAATG CCCAAAGCTC GCCTGACTAC
 251  ATTCCTGATG CTAAATTCTA CAAAGTGGAA GCAATTCTCA GGCCCTGGCG
 301  AGTCTCGCAA GTTTCCTCGG CTTTGCTAAA AATTGGTATT CGAGGTGTTA
 351  CTGTTTCTGA TGTTCGAGGT TTTGGTGCTC AAGGTGGTTC AACTGAGAGG
 401  CAGGGCGGCT CAGAATTTTC TGAAGACAAG TTTGTTGCTA AAGTTAAGAT
 451  GGAGATCGTG GTTAGCAAAG ACCAGGTTGA GGATGTTATA GAAAAAATCA
 501  TTGAGGAGGC AAGAACTGGA GAGATTGGAG ACGGCAAGAT TTTCTTGCTG
 551  CCTGTTTCAG ATGTAATAAG AGTCCGCACT GGTGAGCGGG GTGATAAGGC
 601  TGAGAGGATG ACAGGAGGGC GATCTGACAT GAGTACTTCT GCTTGACTGC
 651  TGTGACCAGC AATATAGCAT TCAGGACTAA CTGTCCTTTG AGAAAGCCCC
 701  GCCCTTATTA GCCATTATCC AGTATAGCTT GATAATTTGA ATTTTTTGTT
 751  TTCTTAACTA AAGAAACAAA GATCTTTTCA TTATCCTGTT GATGATAATT
 801  GAAAACGGAA GGATCGCGAA TTTGTTCAAG TGCTTGCAAG ATAAATAACA
 851  AGAAGAGGAG TAATGTTAAC AAAAAAAAAA AAAAAAAAAA ACTCGAG
```

FIG.13